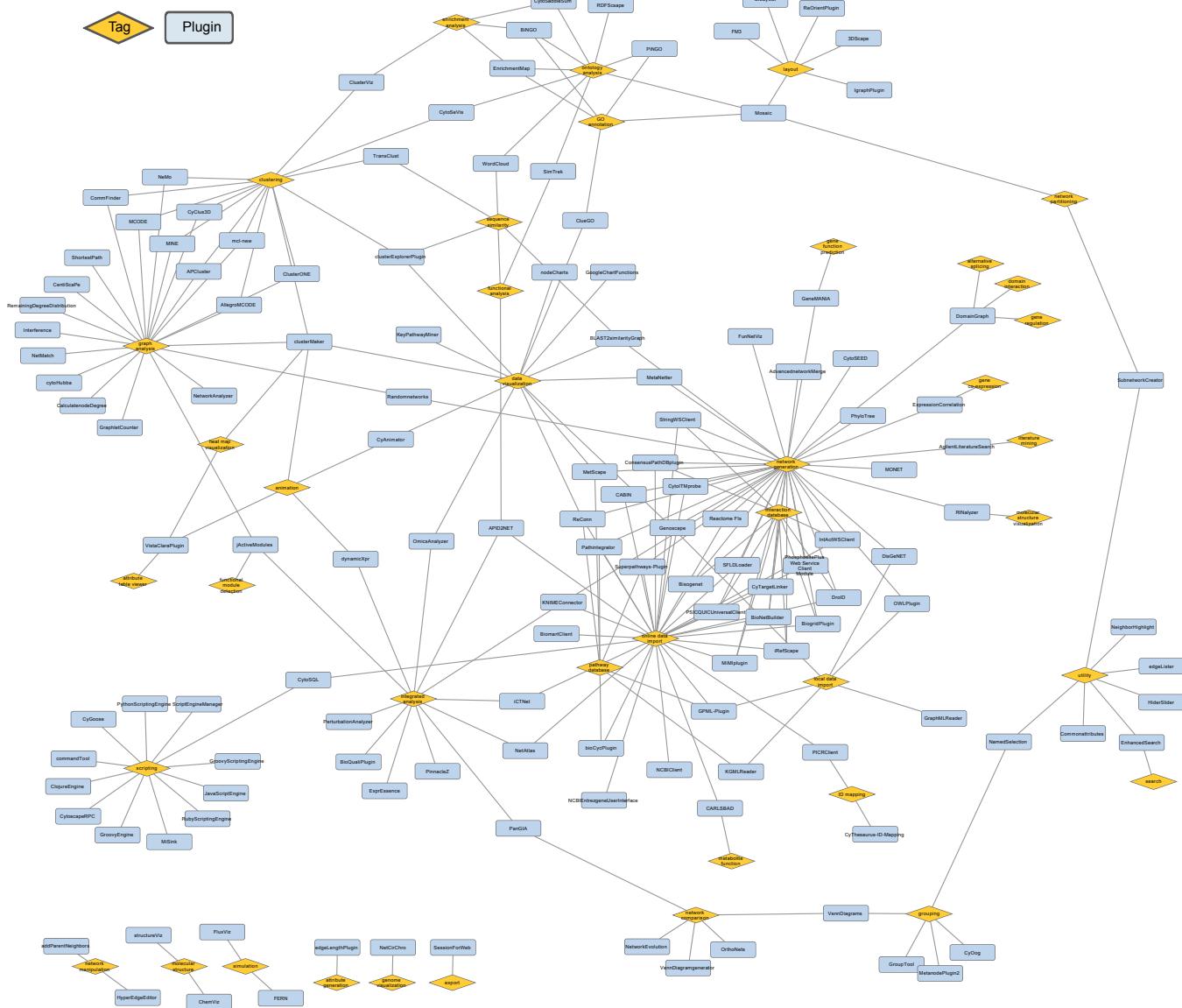
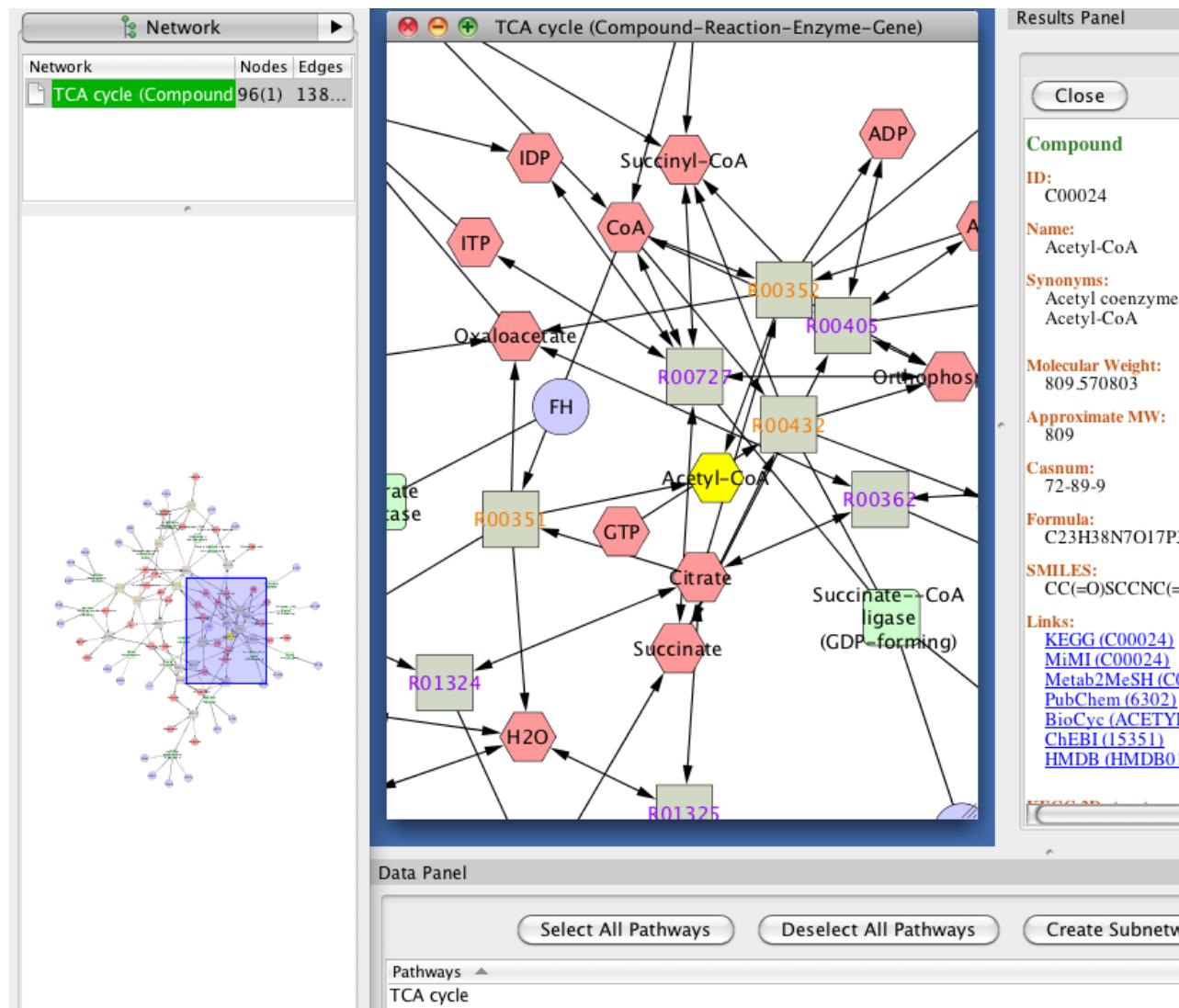


Supplementary Figure 1: Full map of plugin tags.

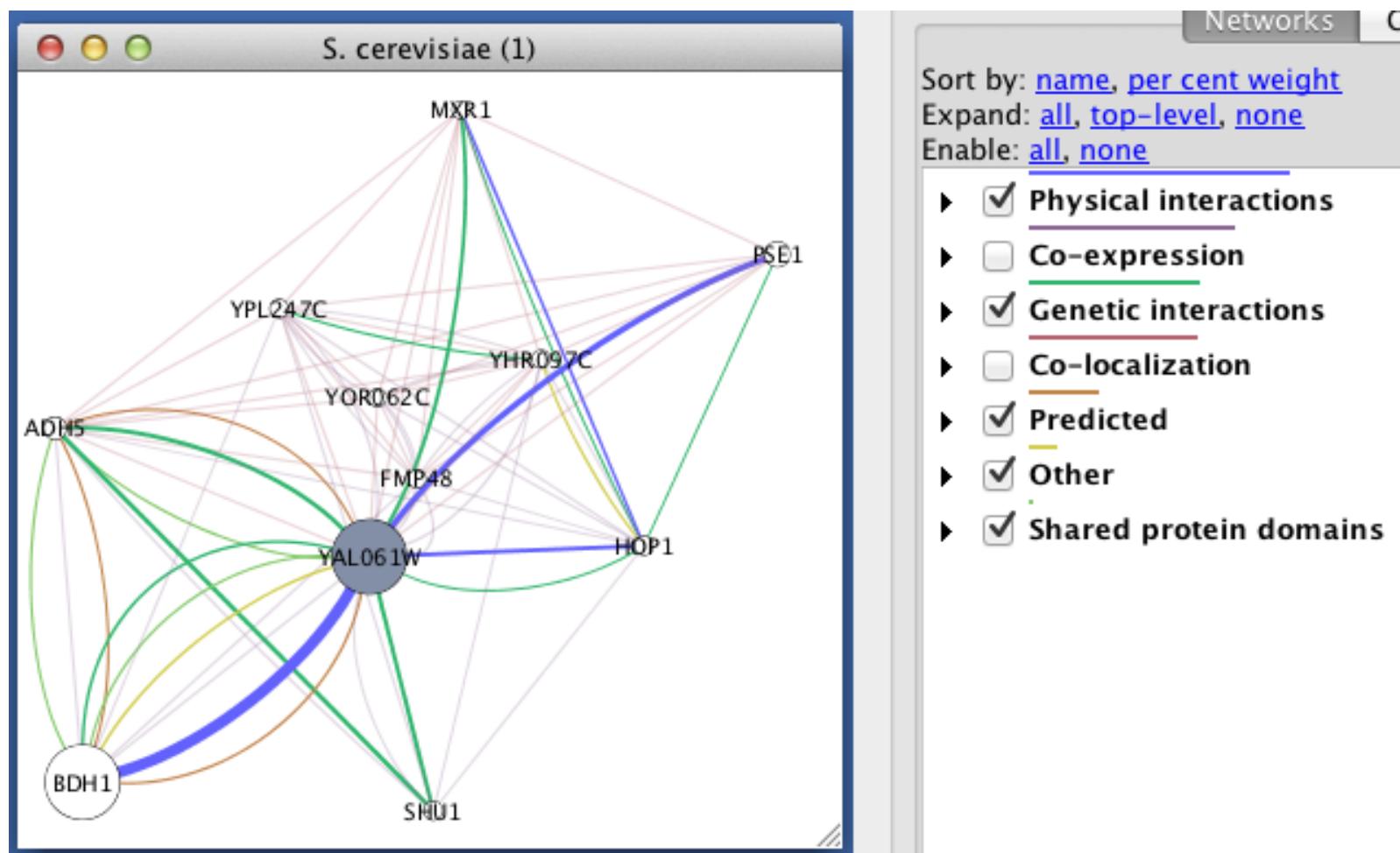


Supplementary Figure 2: Metscape plugin.



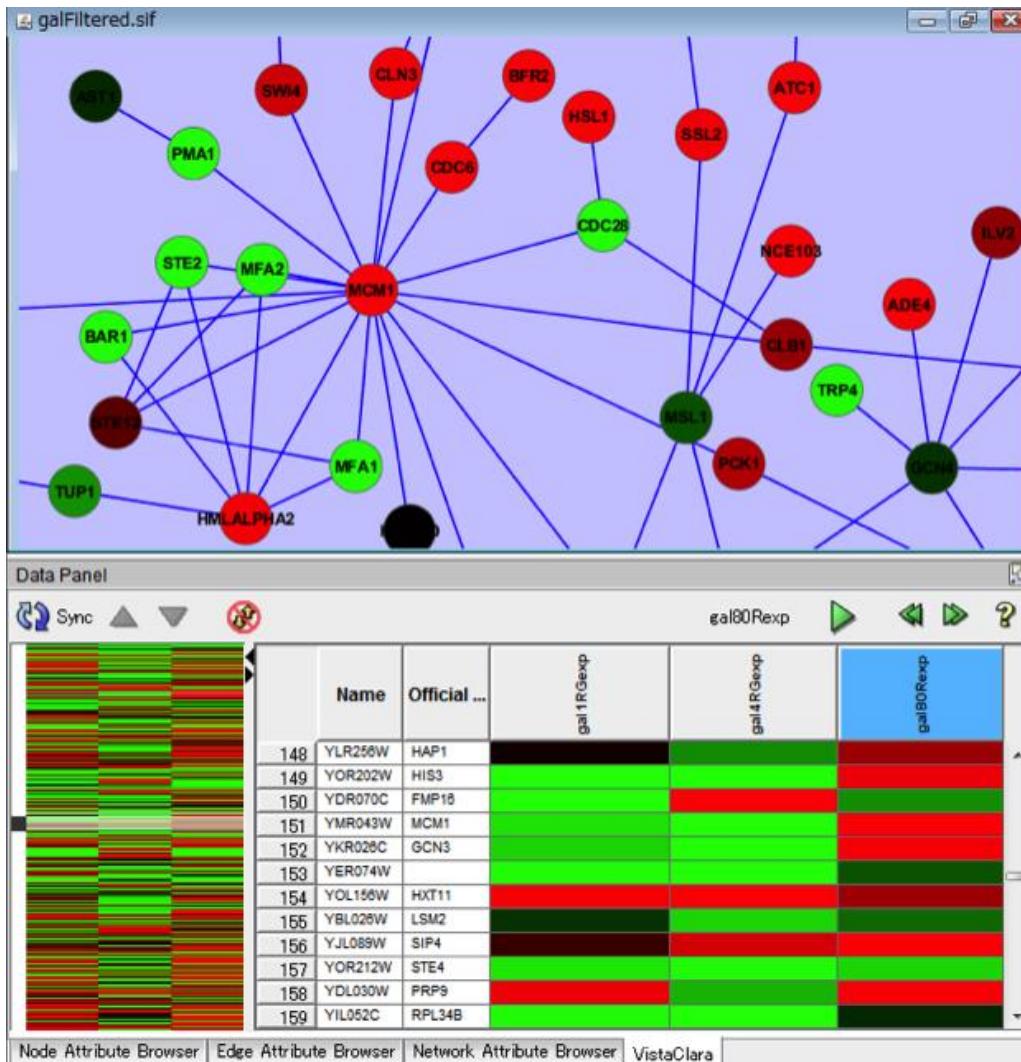
This example shows the human TCA cycle pathway imported using Metscape.

Supplementary Figure 3: The GeneMANIA plugin.



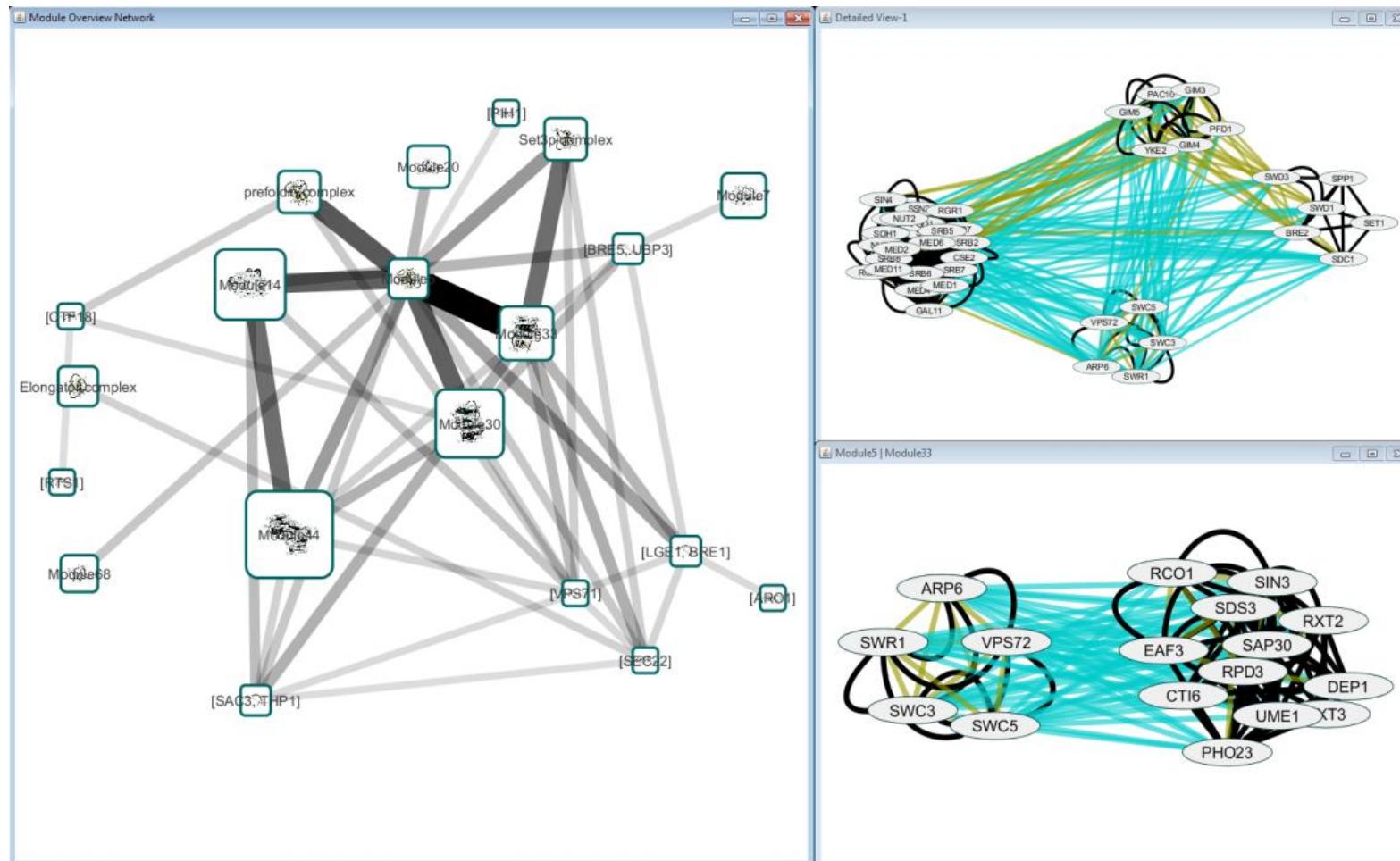
Associations between YAL061W (yeast gene) and other genes are shown. The type of each association is shown on the MANIA Results panel at right.

Supplementary Figure 4: Expression analysis using VistaClaraPlugin.



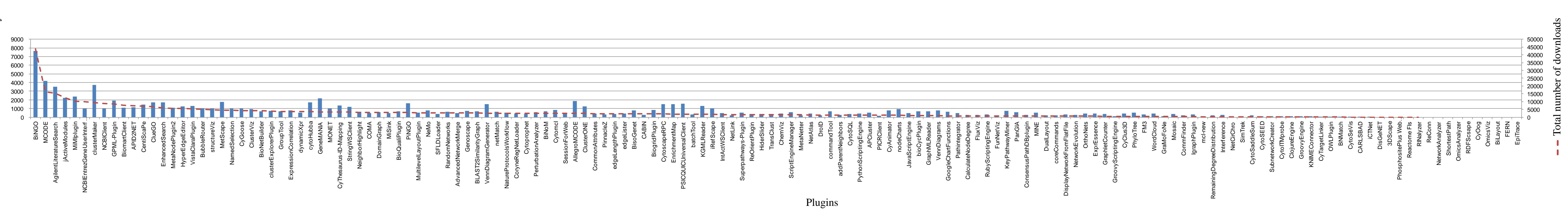
Expression patterns of genes participating in the galactose utilization pathway are displayed as a heat map, and expression at one particular condition is shown by the color of nodes.

Supplementary Figure 5: The PanGIA plugin.



PanGIA clusters genes into modules based on both physical and genetic interactions. In the “Module Overview Network” (left), modules and their genetic interactions are displayed. Detailed gene-level views can also be investigated (right).

Supplementary Figure 6: Number of downloads for all Cytoscape plugins as of April 17, 2012.



Supplementary Table 1: Plugins associated with top ten most common tags. Per category, the two most downloaded plugins are listed. The top ten tags will evolve over time as new tags replace old ones in describing the most common functions and analyses developed for Cytoscape.

Functional tag	Plugins (number of downloads)
Network generation	AgilentLiteratureSearch (15,432); MiMIplugin (10,108)
Online data import	MiMIplugin (10,108); NCBIEntrezGeneUserInterface (10,055)
Graph analysis	MCODE (16,260); jActiveModules (12,547)
Clustering	MCODE (16,260); clusterMaker (9,404)
Data visualization	clusterMaker (9,404); ClueGO (6,681)
Scripting	CyGoose (4,165); MiSink (3,025)
Integrated analysis	jActiveModules (12,547); APID2NET (7,447)
Interaction database	MiMIplugin (10,108); BioNetBuilder (4,060)
Ontology analysis	BiNGO (43,641); Mosaic/BubbleRouter (5,411)
Utility	EnhancedSearch (6,018); NamedSelection (4,416)